OIPE

```
 2 <110> APPLICANT: Suzanne L. Bolten
 3         Alan M. Easton
 4         Leslie C. Engel
 5         Dean M. Messing
 6         John S. Ng
 7         Beverly A. Reitz
 8         Scott A. Vaccaro
 9         Mark C. Walker
10         Ping T. Wang
11         Robin A. Weinberg
13 <120> TITLE OF INVENTION: Aspergillus ochraceus 11 alpha
14        hydroxylase and oxidoreductase
17 <130> FILE REFERENCE: S03196-00-US
C--> 19 <140> CURRENT APPLICATION NUMBER: US/10/021,425
C--> 20 <141> CURRENT FILING DATE: 2001-10-30
22 <150> PRIOR APPLICATION NUMBER: USSN 60/244,300
23 <151> PRIOR FILING DATE: 2000-10-30
25 <160> NUMBER OF SEQ ID NOS: 65
27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 1776
31 <212> TYPE: DNA
32 <213> ORGANISM: Aspergillus ochraceus
34 <220> FEATURE:
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (146)...(1690)
37 <223> OTHER INFORMATION: Aspergillus ochraceus 11 alpha hydroxylase
39 <400> SEQUENCE: 1
40 tggaagtttt tacacttatt atgccggagc cgaaagattc tgagtcgagg ggttggggaa      60
41 caacactata agacctacaa ccacttggat ttggtgaatt tacacgggca ttatcaaaac     120
42 agccacaagc tgacagctca ttatc atg ccc ttc ttc act ggg ctt ctg gcg      172
43                               Met Pro Phe Phe Thr Gly Leu Leu Ala
44                                1               5
46 att tac cat agt ctc ata ctc gac aac cca gtc caa acc ctg agc acc      220
47 Ile Tyr His Ser Leu Ile Leu Asp Asn Pro Val Gln Thr Leu Ser Thr
48 10              15                  20                  25
50 att gtc gta ttg gcg gca gcg tac tgg ctc gca acg ctc cag ccg agc      268
51 Ile Val Val Leu Ala Ala Ala Tyr Trp Leu Ala Thr Leu Gln Pro Ser
52              30                  35                  40
54 gac ctt cct gag ctg aat ccc gcc aaa cca ttc gag ttc acc aat cgt      316
55 Asp Leu Pro Glu Leu Asn Pro Ala Lys Pro Phe Glu Phe Thr Asn Arg
56          45                  50                  55
58 cgt cgt gtt cat gag ttt gtt gaa aat agt aag agc ttg ctt gct cgg      364
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59 Arg Arg Val His Glu Phe Val Glu Asn Ser Lys Ser Leu Leu Ala Arg
60          60              65              70
62 ggg agg gaa ttg cac ggg cac gag ccg tac aga ctc atg tct gaa tgg      412
63 Gly Arg Glu Leu His Gly His Glu Pro Tyr Arg Leu Met Ser Glu Trp
64      75              80              85
66 gga tcc ttg att gtc ctg ccc cca gag tgc gcc gac gag ctg cgc aac      460
67 Gly Ser Leu Ile Val Leu Pro Pro Glu Cys Ala Asp Glu Leu Arg Asn
68 90              95              100             105
70 gac cca aga atg gac ttt gag acg ccc acc acc gac gac tcc cac gga      508
71 Asp Pro Arg Met Asp Phe Glu Thr Pro Thr Thr Asp Asp Ser His Gly
72              110             115             120
74 tat atc cct ggc ttc gac gct ctc aac gca gac ccg aac ctg act aaa      556
75 Tyr Ile Pro Gly Phe Asp Ala Leu Asn Ala Asp Pro Asn Leu Thr Lys
76              125             130             135
78 gtg gtc acc aag tac ctc aca aaa gca ttg aac aag ctt act gct ccg      604
79 Val Val Thr Lys Tyr Leu Thr Lys Ala Leu Asn Lys Leu Thr Ala Pro
80              140             145             150
82 atc tcg cat gaa gcg tcc atc gcc atg aaa gcg gtg ctg ggt gac gat      652
83 Ile Ser His Glu Ala Ser Ile Ala Met Lys Ala Val Leu Gly Asp Asp
84      155             160             165
86 cca gat tgg cgt gag atc tac cca gcc aga gac ttg ctc cag ctc gtc      700
87 Pro Asp Trp Arg Glu Ile Tyr Pro Ala Arg Asp Leu Leu Gln Leu Val
88 170             175             180             185
90 gcc cgg atg tcg aca aga gtg ttc ctt ggc gag gaa atg tgc aat aac      748
91 Ala Arg Met Ser Thr Arg Val Phe Leu Gly Glu Glu Met Cys Asn Asn
92              190             195             200
94 cag gat tgg atc caa acc tca tca caa tac gcg gcc ctt gcc ttc ggt      796
95 Gln Asp Trp Ile Gln Thr Ser Ser Gln Tyr Ala Ala Leu Ala Phe Gly
96              205             210             215
98 gtc ggt gac aag ctt aga ata tac ccg aga atg atc aga ccg ata gta      844
99 Val Gly Asp Lys Leu Arg Ile Tyr Pro Arg Met Ile Arg Pro Ile Val
100             220             225             230
102 cat tgg ttc atg cca tcc tgt tgg gag ctg cgc cga tcg ctg cga cgc     892
103 His Trp Phe Met Pro Ser Cys Trp Glu Leu Arg Arg Ser Leu Arg Arg
104     235             240             245
106 tgc cga cag att ctc acg ccg tac att cac aaa cgc aag tcc ctg aag     940
107 Cys Arg Gln Ile Leu Thr Pro Tyr Ile His Lys Arg Lys Ser Leu Lys
108 250             255             260             265
110 ggg acc acg gac gag cag ggc aag ccc ctt atg ttt gat gat tcc atc     988
111 Gly Thr Thr Asp Glu Gln Gly Lys Pro Leu Met Phe Asp Asp Ser Ile
112             270             275             280
114 gag tgg ttc gag cga gag ctg ggt ccc aac cac gac gcg gtc ctg aag     1036
115 Glu Trp Phe Glu Arg Glu Leu Gly Pro Asn His Asp Ala Val Leu Lys
116             285             290             295
118 cag gtc acg ctc tcc ata gtt gct atc cac acc acg agt gac cta ctc     1084
119 Gln Val Thr Leu Ser Ile Val Ala Ile His Thr Thr Ser Asp Leu Leu
120             300             305             310
122 ttg cag gcc atg agc gat ctc gcg cag aac ccg aaa gtg cta caa gca     1132
123 Leu Gln Ala Met Ser Asp Leu Ala Gln Asn Pro Lys Val Leu Gln Ala
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RAW SEQUENCE LISTING   DATE: 07/22/2002
PATENT APPLICATION: US/10/021,425   TIME: 09:35:07

Input Set : A:\Pto.amc
Output Set: N:\CRF3\07222002\J021425.raw

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124      315                      320                      325
126 gtg cgc gag gag gtg gtc cga gtg ctg agc acc gag ggg ctc agc aag      1180
127 Val Arg Glu Glu Val Val Arg Val Leu Ser Thr Glu Gly Leu Ser Lys
128 330                      335                      340                      345
130 gtc tcg ctt cac agt ctc aag ctc atg gac agc gcg ttg aag gaa agc      1228
131 Val Ser Leu His Ser Leu Lys Leu Met Asp Ser Ala Leu Lys Glu Ser
132                      350                      355                      360
134 cag cgt ctc agg cct acg ctt ctc ggc tcc ttt cgt cgg cag gca acg      1276
135 Gln Arg Leu Arg Pro Thr Leu Leu Gly Ser Phe Arg Arg Gln Ala Thr
136                      365                      370                      375
138 aat gac atc aag ctg aag agc ggg ttt gtc ata aag aaa ggg act aga      1324
139 Asn Asp Ile Lys Leu Lys Ser Gly Phe Val Ile Lys Lys Gly Thr Arg
140           380                      385                      390
142 gtc gtg atc gac agc acc cat atg tgg aat ccc gag tat tac act gac      1372
143 Val Val Ile Asp Ser Thr His Met Trp Asn Pro Glu Tyr Tyr Thr Asp
144      395                      400                      405
146 cct ctc cag tac gac ggg tac cgc tac ttc aac aag cgg cag aca ccc      1420
147 Pro Leu Gln Tyr Asp Gly Tyr Arg Tyr Phe Asn Lys Arg Gln Thr Pro
148 410                      415                      420                      425
150 ggc gag gac aag aac gcg ttg ctc gtc agc aca agc gcc aac cac atg      1468
151 Gly Glu Asp Lys Asn Ala Leu Leu Val Ser Thr Ser Ala Asn His Met
152                      430                      435                      440
154 gga ttc ggt cac ggc gtt cac gcc tgt cct ggc aga ttc ttc gcc tcc      1516
155 Gly Phe Gly His Gly Val His Ala Cys Pro Gly Arg Phe Phe Ala Ser
156                      445                      450                      455
158 aac gag atc aag att gcc ttg tgt cat atc atc tta aat tat gag tgg      1564
159 Asn Glu Ile Lys Ile Ala Leu Cys His Ile Ile Leu Asn Tyr Glu Trp
160           460                      465                      470
162 cgt ctt cca gac ggc ttc aag ccc cag cct ctc aac atc ggg atg act      1612
163 Arg Leu Pro Asp Gly Phe Lys Pro Gln Pro Leu Asn Ile Gly Met Thr
164      475                      480                      485
166 tat ctg gcg gat ccc aat acc agg atg ctg atc agg cca cgc aag gcg      1660
167 Tyr Leu Ala Asp Pro Asn Thr Arg Met Leu Ile Arg Pro Arg Lys Ala
168 490                      495                      500                      505
170 gag atc gat atg gcg agt tta act gtg tag gtcgaacacg aagtcctgat      1710
171 Glu Ile Asp Met Ala Ser Leu Thr Val  *
172                      510
174 gaagtgttat tggtcagtgg gtgaagcaag tcgcagaaat gtgtaacaat ttataagaat      1770
175 aaaaaa                                                                   1776
177 <210> SEQ ID NO: 2
178 <211> LENGTH: 514
179 <212> TYPE: PRT
180 <213> ORGANISM: Aspergillus ochraceus
182 <400> SEQUENCE: 2
183 Met Pro Phe Phe Thr Gly Leu Leu Ala Ile Tyr His Ser Leu Ile Leu
184 1                5                      10                      15
185 Asp Asn Pro Val Gln Thr Leu Ser Thr Ile Val Val Leu Ala Ala Ala
186           20                      25                      30
187 Tyr Trp Leu Ala Thr Leu Gln Pro Ser Asp Leu Pro Glu Leu Asn Pro
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188           35                    40                    45
189 Ala Lys Pro Phe Glu Phe Thr Asn Arg Arg Arg Val His Glu Phe Val
190     50                    55                    60
191 Glu Asn Ser Lys Ser Leu Leu Ala Arg Gly Arg Glu Leu His Gly His
192 65                    70                    75                    80
193 Glu Pro Tyr Arg Leu Met Ser Glu Trp Gly Ser Leu Ile Val Leu Pro
194               85                    90                    95
195 Pro Glu Cys Ala Asp Glu Leu Arg Asn Asp Pro Arg Met Asp Phe Glu
196               100                   105                   110
197 Thr Pro Thr Thr Asp Asp Ser His Gly Tyr Ile Pro Gly Phe Asp Ala
198           115                   120                   125
199 Leu Asn Ala Asp Pro Asn Leu Thr Lys Val Val Thr Lys Tyr Leu Thr
200     130                   135                   140
201 Lys Ala Leu Asn Lys Leu Thr Ala Pro Ile Ser His Glu Ala Ser Ile
202 145               150                   155                   160
203 Ala Met Lys Ala Val Leu Gly Asp Asp Pro Asp Trp Arg Glu Ile Tyr
204               165                   170                   175
205 Pro Ala Arg Asp Leu Leu Gln Leu Val Ala Arg Met Ser Thr Arg Val
206               180                   185                   190
207 Phe Leu Gly Glu Glu Met Cys Asn Asn Gln Asp Trp Ile Gln Thr Ser
208           195                   200                   205
209 Ser Gln Tyr Ala Ala Leu Ala Phe Gly Val Gly Asp Lys Leu Arg Ile
210     210                   215                   220
211 Tyr Pro Arg Met Ile Arg Pro Ile Val His Trp Phe Met Pro Ser Cys
212 225               230                   235                   240
213 Trp Glu Leu Arg Arg Ser Leu Arg Arg Cys Arg Gln Ile Leu Thr Pro
214               245                   250                   255
215 Tyr Ile His Lys Arg Lys Ser Leu Lys Gly Thr Thr Asp Glu Gln Gly
216           260                   265                   270
217 Lys Pro Leu Met Phe Asp Asp Ser Ile Glu Trp Phe Glu Arg Glu Leu
218           275                   280                   285
219 Gly Pro Asn His Asp Ala Val Leu Lys Gln Val Thr Leu Ser Ile Val
220     290                   295                   300
221 Ala Ile His Thr Thr Ser Asp Leu Leu Leu Gln Ala Met Ser Asp Leu
222 305               310                   315                   320
223 Ala Gln Asn Pro Lys Val Leu Gln Ala Val Arg Glu Glu Val Val Arg
224               325                   330                   335
225 Val Leu Ser Thr Glu Gly Leu Ser Lys Val Ser Leu His Ser Leu Lys
226           340                   345                   350
227 Leu Met Asp Ser Ala Leu Lys Glu Ser Gln Arg Leu Arg Pro Thr Leu
228           355                   360                   365
229 Leu Gly Ser Phe Arg Arg Gln Ala Thr Asn Asp Ile Lys Leu Lys Ser
230     370                   375                   380
231 Gly Phe Val Ile Lys Lys Gly Thr Arg Val Val Ile Asp Ser Thr His
232 385               390                   395                   400
233 Met Trp Asn Pro Glu Tyr Tyr Thr Asp Pro Leu Gln Tyr Asp Gly Tyr
234               405                   410                   415
235 Arg Tyr Phe Asn Lys Arg Gln Thr Pro Gly Glu Asp Lys Asn Ala Leu
236           420                   425                   430
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Input Set : A:\Pto.amc
Output Set: N:\CRF3\07222002\J021425.raw

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237 Leu Val Ser Thr Ser Ala Asn His Met Gly Phe Gly His Gly Val His
238         435                 440                 445
239 Ala Cys Pro Gly Arg Phe Phe Ala Ser Asn Glu Ile Lys Ile Ala Leu
240     450                 455                 460
241 Cys His Ile Ile Leu Asn Tyr Glu Trp Arg Leu Pro Asp Gly Phe Lys
242 465                 470                 475                 480
243 Pro Gln Pro Leu Asn Ile Gly Met Thr Tyr Leu Ala Asp Pro Asn Thr
244                 485                 490                 495
245 Arg Met Leu Ile Arg Pro Arg Lys Ala Glu Ile Asp Met Ala Ser Leu
246             500                 505                 510
247 Thr Val
250 <210> SEQ ID NO: 3
251 <211> LENGTH: 2031
252 <212> TYPE: DNA
253 <213> ORGANISM: human
255 <220> FEATURE:
256 <221> NAME/KEY: CDS
257 <222> LOCATION: (1)...(2031)
258 <223> OTHER INFORMATION: human oxidoreductase
260 <400> SEQUENCE: 3
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262 Met Gly Asp Ser His Val Asp Thr Ser Ser Thr Val Ser Glu Ala Val
263 1               5                   10                  15
265 gcc gaa gaa gta tct ctt ttc agc atg acg gac atg att ctg ttt tcg      96
266 Ala Glu Glu Val Ser Leu Phe Ser Met Thr Asp Met Ile Leu Phe Ser
267             20                  25                  30
269 ctc atc gtg ggt ctc cta acc tac tgg ttc ctc ttc aga aag aaa aaa     144
270 Leu Ile Val Gly Leu Leu Thr Tyr Trp Phe Leu Phe Arg Lys Lys Lys
271             35                  40                  45
273 gaa gaa gtc ccc gag ttc acc aaa att cag aca ttg acc tcc tct gtc     192
274 Glu Glu Val Pro Glu Phe Thr Lys Ile Gln Thr Leu Thr Ser Ser Val
275     50                  55                  60
277 aga gag agc agc ttt gtg gaa aag atg aag aaa acg ggg agg aac atc     240
278 Arg Glu Ser Ser Phe Val Glu Lys Met Lys Lys Thr Gly Arg Asn Ile
279 65                  70                  75                  80
281 atc gtg ttc tac ggc tcc cag acg ggg act gca gag gag ttt gcc aac     288
282 Ile Val Phe Tyr Gly Ser Gln Thr Gly Thr Ala Glu Glu Phe Ala Asn
283                 85                  90                  95
285 cgc ctg tcc aag gac gcc cac cgc tac ggg atg cga ggc atg tca gcg     336
286 Arg Leu Ser Lys Asp Ala His Arg Tyr Gly Met Arg Gly Met Ser Ala
287             100                 105                 110
289 gac cct gag gag tat gac ctg gcc gac ctg agc agc ctg cca gag atc     384
290 Asp Pro Glu Glu Tyr Asp Leu Ala Asp Leu Ser Ser Leu Pro Glu Ile
291             115                 120                 125
293 gac aac gcc ctg gtg gtt ttc tgc atg gcc acc tac ggt gag gga gac     432
294 Asp Asn Ala Leu Val Val Phe Cys Met Ala Thr Tyr Gly Glu Gly Asp
295     130                 135                 140
297 ccc acc gac aat gcc cag gac ttc tac gac tgg ctg cag gag aca gac     480
298 Pro Thr Asp Asn Ala Gln Asp Phe Tyr Asp Trp Leu Gln Glu Thr Asp
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/22/2002
PATENT APPLICATION: US/10/021,425   TIME: 09:35:08

Input Set : A:\Pto.amc
Output Set: N:\CRF3\07222002\J021425.raw

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; N Pos. 6,9
Seq#:12; N Pos. 4,10,16